

SEQUENCE LISTING

<110> DIDEBERG, OTTO
VERNET, THIERRY
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES
THEREOF

<130> 70457-19

<140> 10/520,655

<141> 2005-03-07

<150> PCT/IB03/003397

<151> 2003-07-11

<150> FR 02/08724

<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
mini-PBP2x construct

<400> 1

Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Gly Met Glu Ser Ser Leu
35 40 45

Asn Ser Ile Leu Ala Gly Gly Gly Gly Asp Gly Lys Asp Val Tyr Thr
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile
115 120 125



Leu	Tyr	Gln	Ser	Asn	Tyr	Glu	Pro	Gly	Ser	Thr	Met	Lys	Val	Met	Met	130	135	140
Leu	Ala	Ala	Ala	Ile	Asp	Asn	Asn	Thr	Phe	Pro	Gly	Gly	Glu	Val	Phe	145	150	155
Asn	Ser	Ser	Glu	Leu	Lys	Ile	Ala	Asp	Ala	Thr	Ile	Arg	Asp	Trp	Asp	165	170	175
Val	Asn	Glu	Gly	Leu	Thr	Gly	Gly	Arg	Met	Met	Thr	Phe	Ser	Gln	Gly	180	185	190
Phe	Ala	His	Ser	Ser	Asn	Val	Gly	Met	Thr	Leu	Leu	Glu	Gln	Lys	Met	195	200	205
Gly	Asp	Ala	Thr	Trp	Leu	Asp	Tyr	Leu	Asn	Arg	Phe	Lys	Phe	Gly	Val	210	215	220
Pro	Thr	Arg	Phe	Gly	Leu	Thr	Asp	Glu	Tyr	Ala	Gly	Gln	Leu	Pro	Ala	225	230	235
Asp	Asn	Ile	Val	Asn	Ile	Ala	Gln	Ser	Ser	Phe	Gly	Gln	Gly	Ile	Ser	245	250	255
Val	Thr	Gln	Thr	Gln	Met	Ile	Arg	Ala	Phe	Thr	Ala	Ile	Ala	Asn	Asp	260	265	270
Gly	Val	Met	Leu	Glu	Pro	Lys	Phe	Ile	Ser	Ala	Ile	Tyr	Asp	Pro	Asn	275	280	285
Asp	Gln	Thr	Ala	Arg	Lys	Ser	Gln	Lys	Glu	Ile	Val	Gly	Asn	Pro	Val	290	295	300
Ser	Lys	Asp	Ala	Ala	Ser	Leu	Thr	Arg	Thr	Asn	Met	Val	Leu	Val	Gly	305	310	315
Thr	Asp	Pro	Val	Tyr	Gly	Thr	Met	Tyr	Asn	His	Ser	Thr	Gly	Lys	Pro	325	330	335
Thr	Val	Thr	Val	Pro	Gly	Gln	Asn	Val	Ala	Leu	Lys	Ser	Gly	Thr	Ala	340	345	350
Gln	Ile	Ala	Asp	Glu	Lys	Asn	Gly	Gly	Tyr	Leu	Val	Gly	Leu	Thr	Asp	355	360	365
Tyr	Ile	Phe	Ser	Ala	Val	Ser	Met	Ser	Pro	Ala	Glu	Asn	Pro	Asp	Phe	370	375	380
Ile	Leu	Tyr	Val	Thr	Val	Gln	Gln	Pro	Glu	His	Tyr	Ser	Gly	Ile	Gln	385	390	395
Leu	Gly	Glu	Phe	Ala	Asn	Pro	Ile	Leu	Glu	Arg	Ala	Ser	Ala	Met	Lys	405	410	415
Asp	Ser	Leu	Asn	Leu	Gln	Thr	Thr	Ala	Lys	Ala	Leu	Glu	Gln	Val	Ser	420	425	430

Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly
 435 440 445
 Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val
 450 455 460
 Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn
 465 470 475 480
 Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu
 485 490 495
 Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala
 500 505 510
 Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val
 515 520 525
 Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys
 530 535 540
 Ile Thr Leu Thr Leu Gly Asp
 545 550

<210> 2
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 2
 gtcgacttag tctcctaaag ttaatttaat ttttttaatg tttttg

46

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 3
 ggatccggga caggcactcg c

21

<210> 4
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4

cataaatagt cccacgtttg gccccggatc cacgcggaac cag

43

<210> 5

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 5

gtttgggtaa ctacgattgg gacctccaga ggttgcattc tcagcaatcg g

51

<210> 6

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 6

gttcaaggaa ctctccattc caccgccgat aaaactagaa gcaaattg

48

<210> 7

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 7

tgtataaaca tccttacgt cccacctcc ccctgcaaga atactgttc

49

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 8

ccgcatatgg ccaaactgg gactatztat

30

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 9
 ggctcgagtt agtctcctaa agttaatgta at

32

<210> 10
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>
 <221> MOD_RES
 <222> (3)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (4)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (5)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (6)
 <223> Asp or Ser

<220>
 <221> MOD_RES
 <222> (10)..(12)
 <223> variable amino acid

<400> 10
 Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala
 1 5 10

<210> 11
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (1)
 <223> Arg or Lys

<220>
 <221> MOD_RES
 <222> (2)..(3)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (5)
 <223> variable amino acid

<400> 11
 Xaa Xaa Xaa Pro Xaa Gly
 1 5

<210> 12
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (1)
 <223> Gly or Tyr

<220>
 <221> MOD_RES
 <222> (2)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (4)..(6)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (8)..(9)
 <223> variable amino acid

<400> 12
 Xaa Xaa Glu Xaa Xaa Asp Xaa Xaa Leu
 1 5 10

<210> 13
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (1)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (2)..(3)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ser or Thr

<220>
 <221> MOD_RES
 <222> (5)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (7)..(9)
 <223> variable amino acid

<400> 13
 Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln
 1 5 10

<210> 14
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (2)
 <223> Gly or Ser

<220>
 <221> MOD_RES
 <222> (4)..(5)
 <223> hydrophobic amino acid

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<220>
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 <222> (12)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (13)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (14)
 <223> Asp or Asn

<400> 14
 Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa
 1 5 10

<210> 15
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>
 <221> MOD_RES
 <222> (1)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ala or Gly

<220>
 <221> MOD_RES
 <222> (6)..(7)
 <223> variable amino acid

<400> 15
 Xaa Glu Pro Xaa Ser Xaa Xaa Lys
 1 5

<210> 16
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>
 <221> MOD_RES
 <222> (1)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (2)..(3)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (5)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (7)
 <223> hydrophobic amino acid

<400> 16
 Xaa Xaa Xaa Ser Xaa Asn Xaa
 1 5

<210> 17
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 17
 Ala Lys Arg Gly Thr Ile Tyr
 1 5

<210> 18
 <211> 750
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 18
 Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys
 1 5 10 15

Ser	Pro	Ala	Glu	Asn	Arg	Arg	Arg	Val	Gly	Lys	Ser	Leu	Ser	Leu	Leu	20	25	30	
Ser	Val	Phe	Val	Phe	Ala	Ile	Phe	Leu	Val	Asn	Phe	Ala	Val	Ile	Ile	35	40	45	
Gly	Thr	Gly	Thr	Arg	Phe	Gly	Thr	Asp	Leu	Ala	Lys	Glu	Ala	Lys	Lys	50	55	60	
Val	His	Gln	Thr	Thr	Arg	Thr	Val	Pro	Ala	Lys	Arg	Gly	Thr	Ile	Tyr	65	70	75	80
Asp	Arg	Asn	Gly	Val	Pro	Ile	Ala	Glu	Asp	Ala	Thr	Ser	Tyr	Asn	Val	85	90	95	
Tyr	Ala	Val	Ile	Asp	Glu	Asn	Tyr	Lys	Ser	Ala	Thr	Gly	Lys	Ile	Leu	100	105	110	
Tyr	Val	Glu	Lys	Thr	Gln	Phe	Asn	Lys	Val	Ala	Glu	Val	Phe	His	Lys	115	120	125	
Tyr	Leu	Asp	Met	Glu	Glu	Ser	Tyr	Val	Arg	Glu	Gln	Leu	Ser	Gln	Pro	130	135	140	
Asn	Leu	Lys	Gln	Val	Ser	Phe	Gly	Ala	Lys	Gly	Asn	Gly	Ile	Thr	Tyr	145	150	155	160
Ala	Asn	Met	Met	Ser	Ile	Lys	Lys	Glu	Leu	Glu	Ala	Ala	Glu	Val	Lys	165	170	175	
Gly	Ile	Asp	Phe	Thr	Thr	Ser	Pro	Asn	Arg	Ser	Tyr	Pro	Asn	Gly	Gln	180	185	190	
Phe	Ala	Ser	Ser	Phe	Ile	Gly	Leu	Ala	Gln	Leu	His	Glu	Asn	Glu	Asp	195	200	205	
Gly	Ser	Lys	Ser	Leu	Leu	Gly	Thr	Ser	Gly	Met	Glu	Ser	Ser	Leu	Asn	210	215	220	
Ser	Ile	Leu	Ala	Gly	Thr	Asp	Gly	Ile	Ile	Thr	Tyr	Glu	Lys	Asp	Arg	225	230	235	240
Leu	Gly	Asn	Ile	Val	Pro	Gly	Thr	Glu	Gln	Val	Ser	Gln	Arg	Thr	Met	245	250	255	
Asp	Gly	Lys	Asp	Val	Tyr	Thr	Thr	Ile	Ser	Ser	Pro	Leu	Gln	Ser	Phe	260	265	270	
Met	Glu	Thr	Gln	Met	Asp	Ala	Phe	Gln	Glu	Lys	Val	Lys	Gly	Lys	Tyr	275	280	285	
Met	Thr	Ala	Thr	Leu	Val	Ser	Ala	Lys	Thr	Gly	Glu	Ile	Leu	Ala	Thr	290	295	300	
Thr	Gln	Arg	Pro	Thr	Phe	Asp	Ala	Asp	Thr	Lys	Glu	Gly	Ile	Thr	Glu	305	310	315	320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly
 325 330 335
 Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr
 340 345 350
 Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp
 355 360 365
 Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg
 370 375 380
 Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met
 385 390 395 400
 Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu
 405 410 415
 Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu
 420 425 430
 Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser
 435 440 445
 Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala
 450 455 460
 Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile
 465 470 475 480
 Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys
 485 490 495
 Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg
 500 505 510
 Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr
 515 520 525
 Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val
 530 535 540
 Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly
 545 550 555 560
 Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser
 565 570 575
 Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro
 580 585 590
 Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu
 595 600 605
 Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala
 610 615 620

Lys	Ala	Leu	Glu	Gln	Val	Ser	Gln	Gln	Ser	Pro	Tyr	Pro	Met	Pro	Ser	625	630	635	640
Val	Lys	Asp	Ile	Ser	Pro	Gly	Asp	Leu	Ala	Glu	Glu	Leu	Arg	Arg	Asn	645	650	655	
Leu	Val	Gln	Pro	Ile	Val	Val	Gly	Thr	Gly	Thr	Lys	Ile	Lys	Asn	Ser	660	665	670	
Ser	Ala	Glu	Glu	Gly	Lys	Asn	Leu	Ala	Pro	Asn	Gln	Gln	Val	Leu	Ile	675	680	685	
Leu	Ser	Asp	Lys	Ala	Glu	Glu	Val	Pro	Asp	Met	Tyr	Gly	Trp	Thr	Lys	690	695	700	
Glu	Thr	Ala	Glu	Thr	Leu	Ala	Lys	Trp	Leu	Asn	Ile	Glu	Leu	Glu	Phe	705	710	715	720
Gln	Gly	Ser	Gly	Ser	Thr	Val	Gln	Lys	Gln	Asp	Val	Arg	Ala	Asn	Thr	725	730	735	
Ala	Ile	Lys	Asp	Ile	Lys	Lys	Ile	Thr	Leu	Thr	Leu	Gly	Asp			740	745	750	